

JC09 Rec'd PCT/PTO 47 SEP 2005,

SEQUENCE LISTING

<110> Trotta, Christopher R.

<120> TARGETING ENZYMES OF THE tRNA SPLICING
 PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
 ANTI-PROLIFERATIVE MOLECULES

<130> 10589-034-999

<140>

<141> 2004-03-26 (371c date)

<150> PCT/US2004/009590

<151> 2004-03-26

<150> 60/458,067

<151> 2003-03-27

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<223> HsSen2p

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Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
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Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
 35           40           45
Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
 50           55           60
Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
 65           70           75           80
Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
 85           90           95
Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
 100          105          110
Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
 115          120          125
Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
 130          135          140
Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
 145          150          155          160
Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
 165          170          175
Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
 180          185          190
Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
 195          200          205
Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
 210          215          220

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Gln	Asp	Ala	Leu	Ile	Leu	Gln	Arg	Gly	Leu	His	His	Glu	Asp	Gly	Ser
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Gln	His	Ile	Gly	Leu	Leu	His	Pro	Gly	Asp	Arg	Gly	Pro	Asp	His	Glu
				245					250					255	
Tyr	Val	Leu	Val	Glu	Glu	Ala	Glu	Cys	Ala	Met	Ser	Glu	Arg	Glu	Ala
			260					265					270		
Ala	Pro	Asn	Glu	Glu	Leu	Val	Gln	Arg	Asn	Arg	Leu	Ile	Cys	Arg	Arg
		275					280					285			
Asn	Pro	Tyr	Arg	Ile	Phe	Glu	Tyr	Leu	Gln	Leu	Ser	Leu	Glu	Glu	Ala
	290					295					300				
Phe	Phe	Leu	Val	Tyr	Ala	Leu	Gly	Cys	Leu	Ser	Ile	Tyr	Tyr	Glu	Lys
305					310					315					320
Glu	Pro	Leu	Thr	Ile	Val	Lys	Leu	Trp	Lys	Ala	Phe	Thr	Val	Val	Gln
				325					330					335	
Pro	Thr	Phe	Arg	Thr	Thr	Tyr	Met	Ala	Tyr	His	Tyr	Phe	Arg	Ser	Lys
			340					345					350		
Gly	Trp	Val	Pro	Lys	Val	Gly	Leu	Lys	Tyr	Gly	Thr	Asp	Leu	Leu	Leu
		355					360					365			
Tyr	Arg	Lys	Gly	Pro	Pro	Phe	Tyr	His	Ala	Ser	Tyr	Ser	Val	Ile	Ile
	370					375					380				
Glu	Leu	Val	Asp	Asp	His	Phe	Glu	Gly	Ser	Leu	Arg	Arg	Pro	Leu	Ser
385					390					395					400
Trp	Lys	Ser	Leu	Ala	Ala	Leu	Ser	Arg	Val	Ser	Val	Asn	Val	Ser	Lys
				405					410					415	
Glu	Leu	Met	Leu	Cys	Tyr	Leu	Ile	Lys	Pro	Ser	Thr	Met	Thr	Asp	Lys
			420					425					430		
Glu	Met	Glu	Ser	Pro	Glu	Cys	Met	Lys	Arg	Ile	Lys	Val	Gln	Glu	Val
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Ile	Leu	Ser	Arg	Trp	Val	Ser	Ser	Arg	Glu	Arg	Ser	Asp	Gln	Asp	Asp
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Leu															
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<210> 2
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<220>
 <223> HsSen2 variant

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			20					25					30		
Pro	Leu	Lys	Glu	Phe	Lys	Ile	Phe	Arg	Ala	Glu	Met	Ile	Asn	Asn	Asn
		35					40					45			
Val	Ile	Val	Arg	Asn	Ala	Glu	Asp	Ile	Glu	Gln	Leu	Tyr	Gly	Lys	Gly
	50					55					60				
Tyr	Phe	Gly	Lys	Gly	Ile	Leu	Ser	Arg	Ser	Arg	Pro	Ser	Phe	Thr	Ile
65					70					75					80
Ser	Asp	Pro	Lys	Leu	Val	Ala	Lys	Trp	Lys	Asp	Met	Lys	Thr	Asn	Met
				85					90					95	
Pro	Ile	Ile	Thr	Ser	Lys	Arg	Tyr	Gln	His	Ser	Val	Glu	Trp	Ala	Ala
			100					105					110		
Glu	Leu	Met	Arg	Arg	Gln	Gly	Gln	Asp	Glu	Ser	Thr	Val	Arg	Arg	Ile
		115					120					125			
Leu	Lys	Asp	Tyr	Thr	Lys	Pro	Leu	Glu	His	Pro	Pro	Val	Lys	Arg	Asn
	130					135					140				

Glu	Glu	Ala	Gln	Val	His	Asp	Lys	Leu	Asn	Ser	Gly	Met	Val	Ser	Asn
145					150					155					160
Met	Glu	Gly	Thr	Ala	Gly	Gly	Glu	Arg	Pro	Ser	Val	Val	Asn	Gly	Asp
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Ser	Gly	Lys	Ser	Gly	Gly	Val	Gly	Asp	Pro	Arg	Glu	Pro	Leu	Gly	Cys
			180					185							190
Leu	Gln	Glu	Gly	Ser	Gly	Cys	His	Pro	Thr	Thr	Glu	Ser	Phe	Glu	Lys
		195					200					205			
Ser	Val	Arg	Glu	Asp	Ala	Ser	Pro	Leu	Pro	His	Val	Cys	Cys	Cys	Lys
	210					215					220				
Gln	Asp	Ala	Leu	Ile	Leu	Gln	Arg	Gly	Leu	His	His	Glu	Asp	Gly	Ser
225					230					235					240
Gln	His	Ile	Gly	Leu	Leu	His	Pro	Gly	Asp	Arg	Gly	Pro	Asp	His	Glu
				245					250						255
Tyr	Val	Leu	Val	Glu	Glu	Ala	Glu	Cys	Ala	Met	Ser	Glu	Arg	Glu	Ala
			260					265							270
Ala	Pro	Asn	Glu	Glu	Leu	Val	Gln	Arg	Asn	Arg	Leu	Ile	Cys	Arg	Arg
		275					280					285			
Asn	Pro	Tyr	Arg	Ile	Phe	Glu	Tyr	Leu	Gln	Leu	Ser	Leu	Glu	Glu	Glu
	290				295						300				
Pro	Leu	Thr	Ile	Val	Lys	Leu	Trp	Lys	Ala	Phe	Thr	Val	Val	Gln	Pro
305					310					315					320
Thr	Phe	Arg	Thr	Thr	Tyr	Met	Ala	Tyr	His	Tyr	Phe	Arg	Ser	Lys	Gly
				325					330						335
Trp	Val	Pro	Lys	Val	Gly	Leu	Lys	Tyr	Gly	Thr	Asp	Leu	Leu	Leu	Tyr
			340					345					350		
Arg	Lys	Gly	Pro	Pro	Phe	Tyr	His	Ala	Ser	Tyr	Ser	Val	Ile	Ile	Glu
		355					360					365			
Leu	Val	Asp	Asp	His	Phe	Glu	Gly	Ser	Leu	Arg	Arg	Pro	Leu	Ser	Trp
	370				375						380				
Lys	Ser	Leu	Ala	Ala	Leu	Ser	Arg	Val	Ser	Val	Asn	Val	Ser	Lys	Glu
385					390					395					400
Leu	Met	Leu	Cys	Tyr	Leu	Ile	Lys	Pro	Ser	Thr	Met	Thr	Asp	Lys	Glu
			405					410						415	
Met	Glu	Ser	Pro	Glu	Cys	Met	Lys	Arg	Ile	Lys	Val	Gln	Glu	Val	Ile
			420					425					430		
Leu	Ser	Arg	Trp	Val	Ser	Ser	Arg	Glu	Arg	Ser	Asp	Gln	Asp	Asp	Leu
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			20					25					30		
Ser	Trp	Leu	Tyr	Trp	Ala	Tyr	Arg	Tyr	Tyr	Lys	Ser	Thr	Asn	Ala	Leu
		35					40					45			
Asn	Asp	Lys	Val	His	Val	Asp	Phe	Ile	Gly	Asp	Thr	Thr	Leu	His	Ile
	50					55					60				
Thr	Val	Gln	Asp	Asp	Lys	Gln	Met	Leu	Tyr	Leu	Trp	Asn	Asn	Gly	Phe
65					70					75					80
Phe	Gly	Thr	Gly	Gln	Phe	Ser	Arg	Ser	Glu	Pro	Thr	Trp	Lys	Ala	Arg
				85					90					95	

